From:	Angell, Jon E
Sent:	Wednesday, June 02, 2004 4:42 PM
To:	O'Bryen, Barbara
Subject:	Sequence Database Search Request

SEARCH REQUEST FORM
Scientific and Technical Information Center

Examiner# : 78697
Art Unit : 1635
Phone Number: 571-272-0756
Date: 6/2/04
Serial Number: 09/945,173 (Meyers)
Mailbox & Bldg/Room Location: REMSEN 2C18
Results Format Preferred: DISK

I would like to have the following searches performed using the following SEQ. ID NOs. from application : 09/945,173 (Meyers)

SEQ ID NO. 1--nucleic acid sequence (size=~1694 nucleotides)
Please perform: (1) a standard search of SEQ ID NO. 1, as well as
           (2) a search that identifies hits that match SEQ ID NO. 1, but are no longer than 50 nucleotides in length
                (i.e., size limit search wherein the size limit is set to 50 nucleotides)

SEQ ID NO. 2--amino acid sequence encoded by SEQ ID NO. 1 (size=~236 amino acids)
Please perform a search to identify all nucleic acids which encode the amino acid sequence of SEQ ID NO. 2 (i.e., reverse transcribe & search)

Thanks,
Eric

J. Eric Angell
Art Unit 1635
Office: REMSEN 2D20
mailbox: REM 2C18
571-272-0756

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 4, 2004, 19:53:35 ; Search time 6429 Seconds
                                         (without alignments)
                                         11420.610 Million cell
updates/sec

Title: US-09-945-173-1
Perfect score: 1694
Sequence: 1 agggaaggcagtggcaagat..........aaacatgaattattgaacta
1694

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
               1: gb_ba:*
               2: gb_htg:*
               3: gb_in:*
               4: gb_om:*
               5: gb_ov:*
               6: gb_pat:*
               7: gb_ph:*
               8: gb_pl:*
               9: gb_pr:*
               10: gb_ro:*
               11: gb_sts:*
               12: gb_sy:*
               13: gb_un:*
               14: gb_vi:*
               15: em_ba:*
               16: em_fun:*
               17: em_hum:*
               18: em_in:*
               19: em_mu:*
               20: em_om:*
               21: em_or:*
               22: em_ov:*
               23: em_pat:*
               24: em_ph:*
               25: em_pl:*
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               27: em_sts:*
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               29: em_vi:*

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                30:  em_htg_hum:*
                31:  em_htg_inv:*
                32:  em_htg_other:*
                33:  em_htg_mus:*
                34:  em_htg_pln:*
                35:  em_htg_rod:*
                36:  em_htg_mam:*
                37:  em_htg_vrt:*
                38:  em_sy:*
                39:  em_htgo_hum:*
                40:  em_htgo_mus:*
                41:  em_htgo_other:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being
printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1694	100.0	1694	6	AX465669	AX465669
Sequence						
2	1680.6	99.2	3362	9	HSM807705	BX647559 Homo
sapi						
3	1680.6	99.2	3449	9	HSM807739	BX647593 Homo
sapi						
4	1666.8	98.4	1999	9	BC020832	BC020832 Homo
sapi						
5	1660.8	98.0	3352	9	HSM807810	BX647664 Homo
sapi						
6	1387	81.9	2550	9	AK025772	AK025772 Homo
sapi						
7	1022.2	60.3	65838	9	AC133474	AC133474 Homo
sapi						
8	1022.2	60.3	146010	9	AC009289	AC009289 Homo
sapi						
9	875.6	51.7	2064	10	BC050194	BC050194 Mus
muscu						
10	711	42.0	711	6	AX465671	AX465671
Sequence						
11	395.4	23.3	1291	5	AY391440	AY391440
Danio rer						
12	374.8	22.1	385	6	BD076273	BD076273 5'
EST of						
c 13	330.8	19.5	155418	2	AC117754	AC117754 Mus
muscu						
14	321	18.9	321	6	AX906158	AX906158
Sequence						
15	321	18.9	321	6	BD041691	BD041691
Sequence						
16	301.8	17.8	245326	2	AC107288	AC107288
Rattus no						
17	301.8	17.8	266597	2	AC119722	AC119722
Rattus no						
18	139.2	8.2	66009	2	AC101250	AC101250 Mus
muscu						

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      19     135   8.0 119730  9  AC117472              AC117472 Homo
sapi
      20     135   8.0 188485  2  AC027454              AC027454 Homo
sapi
  c   21   102.2   6.0 165836  2  AC138153              AC138153
Danio rer
      22   102.2   6.0 175167  2  BX571724              BX571724
Danio rer
  c   23   102.2   6.0 180928  2  AC139727              AC139727
Danio rer
  c   24    92.6   5.5  66009  2  AC101250              AC101250 Mus
muscu
  c   25    81.6   4.8  87017  2  AC140043              AC140043 Mus
muscu
  c   26    77.6   4.6  29949  2  AC112488              AC112488 Homo
sapi
  c   27    77.6   4.6 179351  2  AC143587              AC143587
Macaca mu
  c   28    67.2   4.0 188485  2  AC027454              AC027454 Homo
sapi
      29    66.8   3.9    934  3  AY070945              AY070945
Drosophil
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Drosophil
      31    56.8   3.4 177577  3  AC022349              AC022349
Drosophil
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Plasmodiu
  c   36    48.2   2.8 134971  2  AC116367              AC116367
Oryza sat
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Oryza sat
  c   38    47.6   2.8 247129  2  AC111725              AC111725
Rattus no
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Dictyoste
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(2 of
      41    46.8   2.8  84550  3  PFMAL1P2_3            Continuation
(4 of
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(19 o
      43    45.8   2.7 131811  9  AC068305              AC068305 Homo
sapi
  c   44    45.8   2.7 136448  2  AC012231              AC012231 Homo
sapi
  c   45    45.8   2.7 138003  2  AC018346              AC018346 Homo
sapi
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ALIGNMENTS

RESULT 1
AX465669

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LOCUS       AX465669                    1694 bp    DNA        linear    PAT 16-
JUL-2002
DEFINITION  Sequence 1 from Patent WO0218425.
ACCESSION   AX465669
VERSION     AX465669.1  GI:21899929
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Meyers,R.A.
  TITLE     47324, a human g-protein and uses therefor
  JOURNAL   Patent: WO 0218425-A 1 07-MAR-2002;
            Millennium Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1. .1694
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             19. .729
                     /note="unnamed protein product"
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                     /db_xref="REMTREMBL:CAD42379"

/translation="MASLDRVKVLVLGDSGVGKSSLVHLLCQNQVLGNPSWTVGCSVD

VRVHDYKEGTPEEKTYYIELWDVGGSVGSASSVKSTRAVFYNSVNGIIFVHDLTNKKS

SQNLRRWSLEALNRDLVPTGVLVTNGDYDQEQFADNQIPLLVIGTKLDQIHETKRHEV

LTRTAFLAEDFNPEEINLDCTNPRYLAAGSSNAVKLSRFFDKVIEKRYFLREGNQIPG
                     FPDRKRFGAGTLKSLHYD"
ORIGIN

  Query Match          100.0%;  Score 1694;  DB 6;  Length 1694;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1694;  Conservative   0;  Mismatches   0;  Indels   0;
Gaps    0;

Qy          1
AGGGAAGGCAGTGGCAAGATGGCGTCCCTGGATCGGGTGAAGGTACTGGTGTTGGGAGAC 60

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Db          1
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Qy         61
TCAGGTGTTGGGAAATCTTCGTTAGTCCATCTCCTATGCCAAAATCAAGTGCTGGGAAAT 120

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Db         61
TCAGGTGTTGGGAAATCTTCGTTAGTCCATCTCCTATGCCAAAATCAAGTGCTGGGAAAT 120


Qy        121
CCATCATGGACTGTGGGCTGCTCAGTGGATGTCAGAGTTCATGATTACAAAGAAGGAACC 180

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Db        121
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Qy        181
CCAGAAGAGAAGACCTACTACATAGAATTATGGGATGTTGGAGGCTCTGTGGGCAGTGCC 240

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Db        181
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Qy        241
AGCAGCGTGAAAAGCACAAGAGCAGTATTCTACAACTCCGTAAATGGTATTATTTTCGTA 300

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Db        241
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Qy        301
CACGACTTAACAAATAAGAAGTCCTCCCAAAACTTGCGTCGTTGGTCATTGGAAGCTCTC 360

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Db        301
CACGACTTAACAAATAAGAAGTCCTCCCAAAACTTGCGTCGTTGGTCATTGGAAGCTCTC 360

Qy        361
AACAGGGATTTGGTGCCAACTGGAGTCTTGGTGACAAATGGGGATTATGATCAAGAACAG 420

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Db        361
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Qy        421
TTTGCTGATAACCAAATACCACTGTTGGTAATAGGGACTAAACTGGACCAGATTCATGAA 480

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Db        421
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Qy        481
ACAAAGCGCCATGAAGTTTTAACTAGGACTGCTTTCCTGGCTGAGGATTTCAATCCAGAA 540

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Db        481
ACAAAGCGCCATGAAGTTTTAACTAGGACTGCTTTCCTGGCTGAGGATTTCAATCCAGAA 540

Qy        541
GAAATTAATTTGGACTGCACAAATCCACGGTACTTAGCTGCAGGTTCTTCCAATGCTGTC 600

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Db        541
GAAATTAATTTGGACTGCACAAATCCACGGTACTTAGCTGCAGGTTCTTCCAATGCTGTC 600

Qy        601
AAGCTCAGTAGGTTTTTTGATAAGGTCATAGAGAAGAGATACTTTTTAAGAGAAGGTAAT 660

|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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AAGCTCAGTAGGTTTTTTGATAAGGTCATAGAGAAGAGATACTTTTTAAGAGAAGGTAAT 660

Qy        661
CAGATTCCAGGCTTTCCTGATCGGAAAAGATTTGGGGCAGGAACATTAAAGAGCCTTCAT 720
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CAGATTCCAGGCTTTCCTGATCGGAAAAGATTTGGGGCAGGAACATTAAAGAGCCTTCAT 720

Qy          721
TATGACTGAATTACACTCATCCTTTGGAAGAGTGAGCAAGCAGTGGCAGTTTTTCACAGC 780

            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          721
TATGACTGAATTACACTCATCCTTTGGAAGAGTGAGCAAGCAGTGGCAGTTTTTCACAGC 780

Qy          781
TCATCTTGCTGTGTTCAATTATTACCATCACAGCCTTTTAACAAAATCATCTTAAAATGC 840

            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          781
TCATCTTGCTGTGTTCAATTATTACCATCACAGCCTTTTAACAAAATCATCTTAAAATGC 840

Qy          841
TACCCTTCAGCCTTACCCTTTAATGGAAAAATGAAAGGAAGTGACAATACGGGAGGTCCA 900

            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          841
TACCCTTCAGCCTTACCCTTTAATGGAAAAATGAAAGGAAGTGACAATACGGGAGGTCCA 900

Qy          901
AACTTTGTCCCTGTTCTCTGTGTTCCTTACCTTTCTGTCCCTGTGTATAGATTATGTAAA 960

            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          901
AACTTTGTCCCTGTTCTCTGTGTTCCTTACCTTTCTGTCCCTGTGTATAGATTATGTAAA 960

Qy          961
AGCCTTGTGTAAATATGAGATGTTGTCAAAATGATGCAGTAAATGAGCAATGACAGTGTA 1020

            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          961
AGCCTTGTGTAAATATGAGATGTTGTCAAAATGATGCAGTAAATGAGCAATGACAGTGTA 1020

Qy          1021
CTGCAGAGAAAATTTACTCTTGCCTAGAACTGGAGGGTTTTTATGGGTCTGTAATTTTCC 1080

            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          1021
CTGCAGAGAAAATTTACTCTTGCCTAGAACTGGAGGGTTTTTATGGGTCTGTAATTTTCC 1080

Qy          1081
CACACTCATTGCTGAAAGCTTAATTAAGTACTTCAAAAACGTATCTCCATTGTTTTACCT 1140

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Db          1081
CACACTCATTGCTGAAAGCTTAATTAAGTACTTCAAAAACGTATCTCCATTGTTTTACCT 1140

Qy          1141
TCTTGAGGGGAACGGTCTTGTTAACCAGCCCTGAGTTGTCTACCCCAAACAATCTCTGTC 1200

            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          1141
TCTTGAGGGGAACGGTCTTGTTAACCAGCCCTGAGTTGTCTACCCCAAACAATCTCTGTC 1200
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Qy        1201
ATTTTCAAAGATGCAAAATGGTGTTATTTAATTGTCTCCACCATTGTCACACACAGGAAT 1260

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Qy        1261
GCCTAATAATAGCAACCCTTGTCTCCCTCTTCTCTCCTTTGCAAATGGCTCAGTGACTGG 1320

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Db        1261
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Qy        1321
AAGAGGCGGACTAATAGCCAGAGTTAAATATAAATACAAATTAATAATACATAGAGAACA 1380

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Db        1321
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Qy        1381
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Qy        1441
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Db        1441
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Qy        1501
TAAGACCTGCACAAGGGCAGTGAGAGACATTTACAGCCTCCTCTCTATTTGTTTTTTTAA 1560

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TAAGACCTGCACAAGGGCAGTGAGAGACATTTACAGCCTCCTCTCTATTTGTTTTTTTAA 1560


Qy        1561
GGAAAAGTCAACTCCTGAAATGTCCCTTAGCTATAATCAGAAAACTAAGAATATTATTCT 1620

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Db        1561
GGAAAAGTCAACTCCTGAAATGTCCCTTAGCTATAATCAGAAAACTAAGAATATTATTCT 1620


Qy        1621
GTGTCAACAATGTATTTATGGAGAGAAGTAAAAATAAGTTCCACAGCAACACAAAAACAT 1680

          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1621
GTGTCAACAATGTATTTATGGAGAGAAGTAAAAATAAGTTCCACAGCAACACAAAAACAT 1680


Qy        1681 GAATTATTGAACTA 1694
               ||||||||||||||
Db        1681 GAATTATTGAACTA 1694
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RESULT 2
HSM807705
LOCUS   HSM807705   3362 bp   mRNA   linear   PRI 30-
AUG-2003
DEFINITION Homo sapiens mRNA; cDNA DKFZp313A1611 (from clone
DKFZp313A1611).
ACCESSION   BX647559
VERSION   BX647559.1 GI:34366716
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 3362)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C.,
Osanger,A.,
            Fobo,G., Han,M. and Wiemann,S.
  CONSRTM   The German Human cDNA Consortium
  TITLE   Direct Submission
  JOURNAL   Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-
85764
            Neuherberg, GERMANY
COMMENT   Clone from S. Wiemann, Molecular Genome Analysis, German
Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by BMFZ (Biomedical Research Center at the
            Heinrich-Heine-University, Duesseldorf/Germany) within the
cDNA
            sequencing consortium of the German Genome Project. This
clone
            (DKFZp313A1611) is available at the RZPD in Berlin. Please
contact
            the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is
available
            at http://mips.gsf.de/proj/cDNA/.
FEATURES   Location/Qualifiers
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host
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     polyA_site   3332
ORIGIN

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Gaps   0;

Qy   1
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Db          10
AGGGAAGGCAGTGGCAAGATGGCGTCCCTGGATCGGGTGAAGGTACTGGTGTTGGGAGAC 69

Qy          61
TCAGGTGTTGGGAAATCTTCGTTAGTCCATCTCCTATGCCAAAATCAAGTGCTGGGAAAT 120

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Db          70
TCAGGTGTTGGGAAATCTTCGTTAGTCCATCTCCTATGCCAAAATCAAGTGCTGGGAAAT 129

Qy         121
CCATCATGGACTGTGGGCTGCTCAGTGGATGTCAGAGTTCATGATTACAAAGAAGGAACC 180

            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         130
CCATCATGGACTGTGGGCTGCTCAGTGGATGTCAGAGTTCATGATTACAAAGAAGGAACC 189

Qy         181
CCAGAAGAGAAGACCTACTACATAGAATTATGGGATGTTGGAGGCTCTGTGGGCAGTGCC 240

            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         190
CCAGAAGAGAAGACCTACTACATAGAATTATGGGATGTTGGAGGCTCTGTGGGCAGTGCC 249

Qy         241
AGCAGCGTGAAAAGCACAAGAGCAGTATTCTACAACTCCGTAAATGGTATTATTTTCGTA 300

            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         250
AGCAGCGTGAAAAGCACAAGAGCAGTATTCTACAACTCCGTAAATGGTATTATTTTCGTA 309

Qy         301
CACGACTTAACAAATAAGAAGTCCTCCCAAAACTTGCGTCGTTGGTCATTGGAAGCTCTC 360

            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         310
CACGACTTAACAAATAAGAAGTCCTCCCAAAACTTGCGTCGTTGGTCATTGGAAGCTCTC 369

Qy         361
AACAGGGATTTGGTGCCAACTGGAGTCTTGGTGACAAATGGGGATTATGATCAAGAACAG 420

            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         370
AACAGGGATTTGGTGCCAACTGGAGTCTTGGTGACAAATGGGGATTATGATCAAGAACAG 429

Qy         421
TTTGCTGATAACCAAATACCACTGTTGGTAATAGGGACTAAACTGGACCAGATTCATGAA 480

            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         430
TTTGCTGATAACCAAATACCACTGTTGGTAATAGGGACTAAACTGGACCAGATTCATGAA 489

Qy         481
ACAAAGCGCCATGAAGTTTTAACTAGGACTGCTTTCCTGGCTGAGGATTTCAATCCAGAA 540

            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         490
ACAAAGCGCCATGAAGTTTTAACTAGGACTGCTTTCCTGGCTGAGGATTTCAATCCAGAA 549

Qy         541
```

```
GAAATTAATTTGGACTGCACAAATCCACGGTACTTAGCTGCAGGTTCTTCCAATGCTGTC 600

        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        Db         550
        GAAATTAATTTGGACTGCACAAATCCACGGTACTTAGCTGCAGGTTCTTCCAATGCTGTC 609


Qy         601
AAGCTCAGTAGGTTTTTTGATAAGGTCATAGAGAAGAGATACTTTTTAAGAGAAGGTAAT 660

        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        Db         610
        AAGCTCAGTAGGTTTTTTGATAAGGTCATAGAGAAGAGATACTTTTTAAGAGAAGGTAAT 669


Qy         661
CAGATTCCAGGCTTTCCTGATCGGAAAGATTTGGGGCAGGAACATTAAAGAGCCTTCAT 720

        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        Db         670
        CAGATTCCAGGCTTTCCTGATCGGAAAGATTTGGGGCAGGAACATTAAAGAGCCTTCAT 729


Qy         721
TATGACTGAATTACACTCATCCTTTGGAAGAGTGAGCAAGCAGTGGCAGTTTTTCACAGC 780

        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        Db         730
        TATGACTGAATTACACTCATCCTTTGGAAGAGTGAGCAAGCAGTGGCAGTTTTTCACAGC 789


Qy         781
TCATCTTGCTGTGTTCAATTATTACCATCACAGCCTTTTAACAAAATCATCTTAAAATGC 840

        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        Db         790
        TCATCTTGCTGTGTTCAATTATTACCATCACAGCCTTTTAACAAAATCATCTTAAAATGC 849


Qy         841
TACCCTTCAGCCTTACCCTTTAATGGAAAAATGAAAGGAAGTGACAATACGGGAGGTCCA 900

        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        Db         850
        TACCCTTCAGCCTTACCCTTTAATGGAAAAATGAAAGGAAGTGACAATACGGGAGGTCCA 909


Qy         901
AACTTTGTCCCTGTTCTCTGTGTTCCTTACCTTTCTGTCCCTGTGTATAGATTATGTAAA 960

        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        Db         910
        AACTTTGTCCCTGTTCTCTGTGTTCCTTACCTTTCTGTCCCTGTGTATAGATTATGTAAA 969


Qy         961
AGCCTTGTGTAAATATGAGATGTTGTCAAAATGATGCAGTAAATGAGCAATGACAGTGTA 1020

        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        Db         970
        AGCCTTGTGTAAATATGAGATGTTGTCAAAATGATGCAGTAAATGAGCAATGACAGTGTA 1029


Qy         1021
CTGCAGAGAAAATTTACTCTTGCCTAGAACTGGAGGGTTTTTATGGGTCTGTAATTTTCC 1080

        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        Db         1030
        CTGCAGAGAAAATTTACTCTTGCCTAGAACTGGAGGGTTTTTATGGGTCTGTAATTTTCC 1089
```

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 4, 2004, 21:11:55 ; Search time 6428 Seconds
                                        (without alignments)
                                        11422.386 Million cell
updates/sec

Title: US-09-945-173-1
Perfect score: 1694
Sequence: 1 agggaaggcagtggcaagat..........aaacatgaattattgaacta
1694

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 1603530

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*
                 15: em_ba:*
                 16: em_fun:*
                 17: em_hum:*
                 18: em_in:*
                 19: em_mu:*
                 20: em_om:*
                 21: em_or:*
                 22: em_ov:*
                 23: em_pat:*
                 24: em_ph:*
                 25: em_pl:*
                 26: em_ro:*
                 27: em_sts:*
                 28: em_un:*
                 29: em_vi:*

```
                     30:  em_htg_hum:*
                     31:  em_htg_inv:*
                     32:  em_htg_other:*
                     33:  em_htg_mus:*
                     34:  em_htg_pln:*
                     35:  em_htg_rod:*
                     36:  em_htg_mam:*
                     37:  em_htg_vrt:*
                     38:  em_sy:*
                     39:  em_htgo_hum:*
                     40:  em_htgo_mus:*
                     41:  em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being
printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	23	1.4	50	6	AR095375	AR095375
Sequence						
c 2	22.6	1.3	50	8	ATH531634	AJ531634
Arabidops						
c 3	22.2	1.3	41	6	AX772159	AX772159
Sequence						
4	22.2	1.3	47	6	AR291819	AR291819
Sequence						
5	22.2	1.3	49	1	AFU430318	AJ430318
Archaeogl						
6	21.8	1.3	41	6	AX515661	AX515661
Sequence						
7	21.8	1.3	41	6	AX518256	AX518256
Sequence						
8	21.8	1.3	47	6	AR291554	AR291554
Sequence						
9	21.6	1.3	42	10	MMU232767	AJ232767 Mus
muscu						
10	21.2	1.3	39	6	AR022583	AR022583
Sequence						
11	21.2	1.3	39	6	AR037598	AR037598
Sequence						
12	21.2	1.3	39	6	AR166584	AR166584
Sequence						
13	21.2	1.3	39	6	AR178056	AR178056
Sequence						
14	21.2	1.3	47	6	AR291096	AR291096
Sequence						
15	20.8	1.2	36	6	AR152139	AR152139
Sequence						
16	20.8	1.2	36	6	AR174546	AR174546
Sequence						
17	20.8	1.2	36	6	AR404212	AR404212
Sequence						
18	20.8	1.2	44	6	AX497105	AX497105
Sequence						

19	20.8	1.2	46	6	I22397	I22397

Sequence 5

c 20	20.8	1.2	47	6	AR291749	AR291749

Sequence

21	20.8	1.2	48	9	S64862S2	S64863 alpha

1-the

22	20.4	1.2	40	6	AR163454	AR163454

Sequence

23	20.4	1.2	40	6	BD103192	BD103192 O-

fucosyl

24	20.4	1.2	40	6	BD103194	BD103194 O-

fucosyl

25	20.4	1.2	45	10	MMC1RNA	X60845

M.musculus

c 26	20.4	1.2	47	6	AR288610	AR288610

Sequence

c 27	20.4	1.2	47	6	AX378249	AX378249

Sequence

c 28	20.4	1.2	47	6	AX378272	AX378272

Sequence

29	20.4	1.2	50	6	AR423115	AR423115

Sequence

30	20.4	1.2	50	6	BD118668	BD118668 EST

and e

31	20.2	1.2	50	6	I36502	I36502

Sequence 1

32	20.2	1.2	50	6	AR423218	AR423218

Sequence

c 33	20.2	1.2	50	6	AX261361	AX261361

Sequence

34	20.2	1.2	50	6	BD118771	BD118771 EST

and e

c 35	20.2	1.2	50	6	BD170451	BD170451

Method of

c 36	20	1.2	28	6	AR014037	AR014037

Sequence

c 37	20	1.2	28	6	I21987	I21987

Sequence 73

38	20	1.2	39	6	AR302247	AR302247

Sequence

39	20	1.2	39	6	AR367377	AR367377

Sequence

40	20	1.2	39	6	AX080330	AX080330

Sequence

41	20	1.2	47	6	I11814	I11814

Sequence 3

42	20	1.2	47	6	BD196579	BD196579

Prostatic

43	20	1.2	50	6	AX164928	AX164928

Sequence

44	20	1.2	50	8	ATH527926	AJ527926

Arabidops

c 45	19.8	1.2	45	6	A67371	A67371

Sequence 12

ALIGNMENTS

RESULT 1
AR095375